

### **REMARKS**

The Office Action dated February 2, 2009 (the first Office Action) did not reject original independent claim 4. Claim 4 was not amended in response to the first Office Action. The outstanding Office Action (the second Office Action) rejects claim 4 under 35 U.S.C. § 112, first and second paragraphs, and also under 35 U.S.C. § 103. Contrary to the outstanding Office Action, none of the new rejections of claim 4 were necessitated by amendment. Claim 4 was not amended prior to the rejections being made. Therefore, the outstanding Office Action should not have been made final. Withdrawal of the finality of the outstanding Office Action is respectfully requested.

The present invention relates to a method that includes the steps of obtaining amino acid sequences, preferably amino acid sequences of peptides (Fig. 1(c)), estimating a mass for each of the sequences (Fig. 1(d)), and calculating a number of occurrences for each of the estimated masses (Fig. 1(e)). The sequences (Fig. 1(c)) are obtained from protein information that is stored in a database (Fig. 1(a)). Then, after the occurrence numbers are calculated, an apparatus (Fig. 3) is used (Fig. 1(g)) to obtain a mass spectrum of a sample (Fig. 1(h)), and then, a precursor ion is selected based on the occurrence numbers and the mass spectrum (Fig. 1(k)). Please refer, for example, to the specification ¶¶ 0055-0062 (describing the use of frequency information, represented as  $W_m$ , and information extracted from the  $MS^1$  analysis, represented as  $E_m$ ).

Claims 1-11 are rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. Reconsideration is respectfully requested. Independent claims 1 and 8 have been amended to refer to plural amino acid sequences. Independent claim 4 has been amended to refer to estimating masses of peptides. The rejection of dependent claim 6 is not understood. Claim 6 is an original claim, and “original claims constitute their own description.” In re Koller, 613 F.2d 819, 823 (CCPA 1980). As explained in M.P.E.P. § 608.01(l), “[an original] claim should not be attacked either by objection or rejection” on grounds that “[its] subject matter is lacking in the drawing and description.”

Claims 1-11 are rejected under 35 U.S.C. § 112, second paragraph, as being “incomplete.” Reconsideration is respectfully requested. The Office Action reads the claims too narrowly. Claims 1-3 do not say that the recited “sample” cannot be digested. Claims 4-7 and 11 do not exclude the step of “digestion of [a] protein sample.” Similarly, claims 8-10 refer broadly to “mass analysis of an actual sample.” All of the claims are broader in scope than the preferred embodiments, and they should not be limited to the preferred embodiments. As explained in the specification ¶ 0096, digestion is optional in certain embodiments of the invention.

Claims 1-11 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. Reconsideration is respectfully requested. Method claim 1 has been amended to recite the step of “estimating a mass for each of [a plurality of] amino acid sequences.” The claim is not limited to any specific group of sequences. Claim 5 has been amended as helpfully suggested by the Office Action. Claim 8 has been amended to say that “a mass is estimated for each of [plural] amino acid sequences.” As with claim 1, claim 8 is not limited to any specific sequences. The Office Action’s concerns with respect to independent claim 4 and dependent claims 7 and 11, if any, are not stated and are not understood. All of the claims, as amended, are believed to be in full compliance with 35 U.S.C. § 112.

Claims 1, 2 and 8 are rejected under 35 U.S.C. § 102 as being anticipated by Reid. Claims 3, 4, 7 and 9-11 are rejected under 35 U.S.C. § 103 as being unpatentable over Reid. Reconsideration is respectfully requested. The Office Action, page 7, cites paragraphs 2 and 3 in the right column of Reid page 664, and paragraph 1 on page 665, as teaching all elements of claim 1. In these three paragraphs, Reid teaches two approaches to protein analysis. First, Reid teaches a conventional mass spectrometry approach in which masses of extracted peptides are analyzed to form a peptide “mass fingerprint” which can be used in database searches to identify a protein. Reid at page 664, right column, paragraph 2. Next, Reid teaches “a more comprehensive protein analysis approach” in which each of the peptides are subjected to tandem mass spectrometry (MS/MS). Reid at page 665, right column, paragraph 3. This section goes on to describe various mass spectrometry technologies that could be applied, and problems with the general analysis

strategy. In this second section, Reid merely presents that the peptides extracted via enzymatic digestion can be subjected to MS/MS analysis.

Reid fails to disclose or suggest the steps of “[1] calculating a number of occurrences for each of [plural] masses; [2] subsequently, obtaining a mass spectrum by performing an MS analysis of a sample . . . [and] [3] selecting a precursor ion based on the . . . mass spectrum and the calculated numbers of occurrences.” These are important aspects of the invention of claim 1, as amended. Therefore, claim 1, as amended, should be allowable over Reid. Claims 2 and 3 depend from claim 1 and should be allowable along with claim 1 and for other reasons.

Reid only discusses methods of determining the masses of peptides, and only in general terms. At no point does Reid teach or suggest that, once the mass of the peptide is determined, a number of amino acid sequences with a given mass is calculated. Nor does Reid teach or suggest that this calculation is used along with the result of an MS analysis, to select a precursor ion (an ion to be fragmented). Moreover, Reid does not teach subjecting a precursor ion to MS/MS analysis or performing an identification process using the mass spectrum obtained through this analysis.

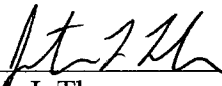
Claim 4, as amended, recites the steps of “normalizing the spectrum of [a] sample such that 1 is given for each mass, when there is a mass, and 0 is given when there is no mass.” Support for the amendment appears in the original disclosure, for example, in connection with Fig. 1(i). Reid fails to disclose or suggest this important aspect of the claimed invention. Even if it would have been obvious to normalize a sample spectrum, a point which is not conceded, it would not have been obvious to assign 1 to each mass where there is a mass, and 0 where there is no mass. Claims 5-7 and 11 depend from claim 4 and should be allowable along with claim 4 and for other reasons.

Claims 8-10 recite limitations that are similar, though not identical, to those discussed above in connection with claim 1. Claims 8-10 should be allowable along with claim 1 and for other reasons.

Allowance of the application, as amended, with claims 1-11, is solicited.

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